

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jiang, Min
 Potter, Andrew A.
 - MacLachlan, Philip R.
- (ii) TITLE OF INVENTION: CAMP FACTOR OF STREPTOCOCCUS UBERIS
- (iii) NUMBER OF SEQUENCES: 4
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Reed & Robins LLP
 - (B) STREET: 285 Hamilton Avenue, Suite 200
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94301
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/658,277
 - (B) FILING DATE: 05-JUN-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Robins, Roberta L.
 - (B) REGISTRATION NUMBER: 33,208
 - (C) REFERENCE/DOCKET NUMBER: 9000-0030
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 327-3400
 - (B) TELEFAX: (415) 327-3231
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) IFNGTH: 1191 base pairs
 - (ii) MOLECULE TYPE: DNA (genomic)

(ix)	FEATURE:
(+ 3.	,

(A) NAME/KEY: CDS

(B) LOCATION: 157..924

(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:1:
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(XI) SE	ZULNCL DEBC.	(11 11 011 1	DEQ ID NO						
AATGAACATA	TAAAAATAAA	CATTAATAAT	TTTTATA 7	TAT	GATAATC	ACA T	ATAT	TTGAC	60
ТТАААААААТ	rgttactgta '	rgatacagg(C ATAAGTA	ACTT Z	ATTTATT	TTA T	AGAT	TGCAA	120
TTTATAAACA	TTTATATTT	ΓCAAAGAGG <i>l</i>	A ATGCTT	ATG (Met (GAA TTC Glu Phe	AAA Lys	AAG Lys 5	TTA Leu	174
CTT TAT TTA Leu Tyr Leu	ACT GGT TC Thr Gly Se 10	A ATC GCA	GGA ATT Gly Ile 15	ACT Thr	TTA TTT Leu Phe	TCC Ser 20	CCA Pro	ATT Ile	222
TTA ACA AGT Leu Thr Ser 25	GTC CAA GC Val Gln Al	A AAT CAA a Asn Gln 30	ATA AAT Ile Asn	GTT . Val	AGT CAA Ser Gln 35	Pro	TCT Ser	AAT Asn	270
AAT GAA AGT Asn Glu Ser 40	AAT GTT AT Asn Val Il	T TCA CAG e Ser Gln 45	AAA AAA Lys Lys	GAA Glu	GAA ATT Glu Ile 50	GAT Asp	AAT Asn	AGT Ser	318
CTA AAT CAG Leu Asn Gln 55	GAA AGT GC Glu Ser Al 6	a Gln Leu	TAT GCC Tyr Ala	TTG Leu 65	AAA GAA Lys Glu	GAT Asp	GTT Val	AAA Lys 70	366
GGA ACT GAG Gly Thr Glu	AAA GAA CA Lys Glu Gl 75	A TCA GTT n Ser Val	AAT TCA Asn Ser 80	GCA Ala	ATT TCA	GCT Ala	GTT Val 85	GAA Glu	414
AAT TTA AAA Asn Leu Lys	ACT TCA CT Thr Ser Le	T AGA GCT u Arg Ala	AAT CCT Asn Pro 95	GAA Glu	ACA ATT	TAT Tyr 100	GAT Asp	TTA Leu	462
AAT TCG ATT Asn Ser Ile 105	Gly Thr Ar	A GTA GAA g Val Glu 110	GCA ATC Ala Ile	TCT Ser	GAC GTO Asp Val	Ile	CAA Gln	GCA Ala	510
ATT GTT TTT	TCA ACG CA Ser Thr Gl	A CAG TTA n Gln Leu	ACA AAT Thr Asn	AAA Lys	GTT GAT Val Asp	CAA Gln	GCT Ala	CAC His	558

CCA TTT GCT TCA AAT GAA TCC ATT AAA GGG CAA GTC GAA GCT GTT AAA Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly Gln Val Glu Ala Val Lys 155 160 165	654
CAA GTG CAA GCG ACT GTG CTT ACC TAT CCC GAT TTG CAG CCT ACG GAT Gln Val Gln Ala Thr Val Leu Thr Tyr Pro Asp Leu Gln Pro Thr Asp 170	702
AGA GCA ACT ATT TAC GTT AAA TCA AAA TTA GAC AAG CTT ATT TGG CAA Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu Asp Lys Leu Ile Trp Gln 185 190 195	750
ACA AGA ATT ACC AGA GAT CAA AAA GTT CTT AAT GTA AAG AGT TTT GAA Thr Arg Ile Thr Arg Asp Gln Lys Val Leu Asn Val Lys Ser Phe Glu 200 205 210	798
GTT TAT CAT CAA TTA AAT AAA GCT ATC ACA CAT GCA GTA GGT GTA CAA Val Tyr His Gln Leu Asn Lys Ala Ile Thr His Ala Val Gly Val Gln 215 220 225 230	846
TTA AAT CCA ACT GTA ACA GTT GCA CAA GTT GAC CAA GAA ATC AAA GTG Leu Asn Pro Thr Val Thr Val Ala Gln Val Asp Gln Glu Ile Lys Val 235 240 245	894
CTA CAA GAA GCA TTA AAT ACT GCT CTA CAG TAAGGTAGAG ATTGAATTGA	944
CGTATTAAAA AGGACTGGAA TTTATTAATT TCAGTCCTTT AGAATTTTTA TTTAGCTGAT	1004
TTACTTGTTG AAGAGATTTG GTGGAAAATC AAGTACCATA CTTCATTTCT CCTCCAAATA	1064
CTTGTATGTC GATTCCCTTC TAAAACATAG CTAATTAGTT TAGTTTTCTG GCTAATAGAT	1124
TGTACATGAA ATTGTTCAAA ATTACTAGGG TAAAAGGTTT TTCTTTTTAT AAATTCATCA	1184
TGACTAT	1191

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 amino acids
 - (B) TYPE: amino acid (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Lys Lys Leu Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala Asn Gln Ile Asn 25 Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala 50 Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro 90 Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg Val Glu Ala Ile 100 105 Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn 120 115 Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu 135 Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly 160 150 145 Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro 170 165 Asp Leu Gln Pro Thr Asp Arg Ala Thr Ile Tyr Val Lys Ser Lys Leu 185 Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu 200 195 Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr 220 215 210 His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val 240 235

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
- Met Glu Phe Lys Lys Leu Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile 1 5 10 15
- Thr Leu Phe Ser Pro Ile Leu Thr Ser Val Gln Ala Asn Gln Ile Asn 20 25 30
- Val Ser Gln Pro Ser Asn Asn Glu Ser Asn Val Ile Ser Gln Lys Lys 35 40 45
- Glu Glu Ile Asp Asn Ser Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala 50 55 60
- Leu Lys Glu Asp Val Lys Gly Thr Glu Lys Glu Gln Ser Val Asn Ser 65 70 75 80
- Ala Ile Ser Ala Val Glu Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro 85 90 95
- Glu Thr Ile Tyr Asp Leu Asn Ser Ile Gly Thr Arg Val Glu Ala Ile 100 105 110
- Ser Asp Val Ile Gln Ala Ile Val Phe Ser Thr Gln Gln Leu Thr Asn 115 120 125
- Lys Val Asp Gln Ala His Ile Asp Met Gly Phe Ala Ile Thr Lys Leu 130 135 140
- Leu Ile Arg Ile Ala Asp Pro Phe Ala Ser Asn Glu Ser Ile Lys Gly
 145 150 155 160
- Gln Val Glu Ala Val Lys Gln Val Gln Ala Thr Val Leu Thr Tyr Pro

Asp Lys Leu Ile Trp Gln Thr Arg Ile Thr Arg Asp Gln Lys Val Leu 195 200 205

Asn Val Lys Ser Phe Glu Val Tyr His Gln Leu Asn Lys Ala Ile Thr 210 215 220

His Ala Val Gly Val Gln Leu Asn Pro Thr Val Thr Val Ala Gln Val 225 230 235 240

Asp Gln Glu Ile Lys Val Leu Gln Glu Ala Leu Asn Thr Ala Leu Gln 245 250 255

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Gln Val Thr Thr Pro Gln Val Val Asn His Val Asn Ser Asn Asn 1 5 10 15

Gln Ala Gln Gln Met Ala Gln Lys Leu Asp Gln Asp Ser Ile Gln Leu 20 25 30

Arg Asn Ile Lys Asp Asn Val Gln Gly Thr Asp Tyr Glu Lys Pro Val

Asn Glu Ala Ile Thr Ser Val Glu Lys Leu Lys Thr Ser Leu Arg Ala 50 55 60

Asn Ser Glu Thr Val Tyr Asp Leu Asn Ser Ile Gly Ser Arg Val Glu 65 70 75 80

Ala Leu Thr Asp Val Ile Glu Ala Ile Thr Phe Ser Thr Gln His Leu 85 90 95

Lys Leu Var Tre Arg III II a noperform of the File 115 120 125

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Lys Ala Gln Val Asn Asp Val Lys Ala Leu Glu Gln Lys Val Leu Thr 130 135 140

Tyr Pro Asp Leu Lys Pro Thr Asp Arg Ala Thr Ile Tyr Thr Lys Ser 145 150 155 160

Lys Leu Asp Lys Glu Ile Trp Asn Thr Arg Phe Thr Arg Asp Lys Lys 165 170 175

Val Leu Asn Val Lys Glu Phe Lys Val Tyr Asn Thr Leu Asn Lys Ala 180 185 190

Ile Thr His Ala Val Gly Val Gln Leu Asn Pro Asn Val Thr Val Gln 195 200 205

Gln Val Asp Gln Glu Ile Val Thr Leu Gln Ala Ala Leu Gln Thr Ala 210 215 220

Leu Lys 225